

FIG. 1A

1 CTGCTTCCACAGCAAGACACGACTGGAGAGCCGAGCCGGAGCAGCTGGGAACATG 60
 -----+-----+-----+-----+-----+-----+
 GACGAAGGTGCTGTTCTGCTGACCTCTCGGCTCGGCCCTCGTCGACCCCTTTGTAC M

61 AAGAGCGTCTTGCTGCTGACACGCTCCTCGTGCCTGCACACCTGGTGGCCGCTGGAGC 120
 -----+-----+-----+-----+-----+-----+
 TTCTCGCAGAACGACGACTGCTGCGAGGAGCAGGACGTGTGACCACCGGGACCTCG
 K S V L L L T T L L V P A H L V A A W S

121 AATAATTATGCGGTGACTGCCCTCAACACTGTGACAGCAGTGAGTGCAAAAGCAGCCCG 180
 -----+-----+-----+-----+-----+-----+
 TTATTAATACGCCACCTGACGGGAGTTGTGACACTGTCTGCTACTCAGCTTTTCGTGGGC
 N N Y A V D C P Q H C D S S E C K S S P

181 CGCTGCAAGAGGACAGTGTCTCGACGACTGTGGCTGTCTGCCGAGTGTGCCGTGCAGGGCGG 240
 -----+-----+-----+-----+-----+-----+
 GCGACGTTCTCCTGTACGAGCTGCTGACACCGACGCGGCTCACACGCGACGTCCCGCC
 R C K R T V L D D C C G C C R V C A A G R

MATCH WITH FIG. 1B

FIG. 1B

MATCH WITH FIG. 1A

241 GGAGAACTTGCTACCGCACAGTCTCAGGCATGGATGGCATGAAGTGTGCCCGGGGCTG
 ---+---+---+---+---+---+---+---+---+---+---+---+---+
 CCTCTTTGAACGATGGCGTGTGAGAGTCCGTACCTACCGTACTTCACACCCGGCCCCGAC
 G E T C Y R T V S G M D G M K C G P G L 300

301 AGGTGTCAGCCTTCTAATGGGAGGATCCTTTTGGTGAAGAGTTTGGTATCTGCCAAAGAC
 ---+---+---+---+---+---+---+---+---+---+---+---+---+
 TCCACAGTCGGAAGATTACCCCTCCTAGGAAACCACCTTCTCAACCATAGACGTTTCTG
 R C Q P S N G E D P F G E E F G I C K D 360

361 TGTCCCTACGGCACCTTCGGGATGGATTCAGAGAGACCTTGCAACTGCCAGTCAGGCATC
 ---+---+---+---+---+---+---+---+---+---+---+---+---+
 ACAGGGATGCCGTGGAAGCCCTACCTAACGTCCTCTCTGACGTTGACGGTCAGTCCGTAG
 C P Y G T F G M D C R E T C N C Q S G I 420

421 TGTGACAGGGGACGGGAAATGCCTGAAATTCCTCCCTTCTTCCAAATATCAGTAACCAAG
 ---+---+---+---+---+---+---+---+---+---+---+---+---+
 AACTGTCCCCCTGCCCTTTTACGGACTTTAAGGGAAGAAGTTATAAGTCATTGGTTC
 C D R G T G K C L K F P F Q Y S V T K 480

MATCH WITH FIG. 1C

FIG. 1C

MATCH WITH FIG. 1B

481 TCTTCCAACAGATTGTCTCTCACCAGGAGCATGACATGGCATCTGGAGATGGCAATATT
 540 -----+-----+-----+-----+-----+-----+-----+
 AGAAGGTTGTCTAAACAAGAGAGTGCCCTCGTACTGTACCGTAGACCCTCTACCGTTATAA
 S S N R F V S L T E H D M A S G D G N I

541 GTGAGAGAAGATTGTGAAGAGAATGCTGCCGGTCTCCCGTAATGAGGAAATGGTTA
 -----+-----+-----+-----+-----+-----+-----+
 CACTCTCTTCAACACTTTCTCTTACGACGGCCAGAGGGCATTTACTCCTTTACCAAT
 V R E E V V K E N A A G S P V M R K W L

601 AATCCACGCTGATCCCCGGCTGTGATTCTTGAGAGAAGGCTCTATTTCGTGAYTGTTCAA
 -----+-----+-----+-----+-----+-----+-----+
 TTAGGTGCGACTAGGGCCGACACTAAAGACTCTCTCCGAGATAAAGCAGCCTRACAACTT
 N P R *

661 CACACAGCCAACATTTAGGAACCTTCTAGATTATAGCATAAGGACATGTAATTTTGAA
 -----+-----+-----+-----+-----+-----+-----+
 GTGTGTCGGTTGTAAATAATCCTTGAAAGATCTAATATCGTATTCTGTACATTAAAAACTT

721 GACCAAAATGTGATGCATGGTGATCCAGAAACAAAGTAGGATACTTACAATCCATAA
 -----+-----+-----+-----+-----+-----+-----+
 CTGGTTACACTACGTACCACCTAGGTCTTTGTGTTTTCATCCTATGAATGTTAGGTATT

MATCH WITH FIG. 1D

MATCH WITH FIG. 1C

781

841

106

961

1021

MATCH WITH FIG. 1E

32-500-204

1140

1081

1200

1141

1260

1201

1261

1271

ce10_chick	1	..MGSAGAR	P.ALAAALLC	LARLALGSPC	PAV.....CQC	...PAA.APQ
cyr6_mouse		..MSSSTFR	TLAVAVTLAH	LTRLAL.STC	PAA.....CHC	...PLE.APK
ctgf_human		..MTAASMPV	RVAFVLLAL	CSRPAVGQNC	SGP.....CRC	...PDEPAPR
fisp-12		..MLASVAGPI	SLAL.VLLAL	CTRATGQDC	SAQ.....CQC	...AAEAAPH
nov_chick		..METGGGQGL	PVLLLLLLLL	RPCEVSGREA	ACPRPCGGRC	...PAEP.PR
ibp_3human		MQRARPTLWA	AALTLLVLLR	GPPVARAGAS	SGGLGPVVRC	EPCVARALAR
ccn-4	MK	SVLLLTTLV	PAHLVAAWSN	MYAVDCPQHC	DSSECKSSPR

	51	100
ce10_chick	CAPGVGLVP. DCGCC KCAKQLNED C.... SRTQP	CDHTKGLECN
cyr6_mouse	CAPGVGLVR. DCGCC KCAKQLNED C.... SKTQP	CDHTKGLECN
ctgf_human	CPAGVSLVL. DCGCC RCAKQLGEL C.... TERDP	CDPHKGLFCD
ccn-4

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401      411
ce10_chick      RLVNDIHKFR D
cyr6_mouse      SLFNDIHKFR D
ctgf_human      YYRKMVGDMA .
fisp-12         YYRKMVGDMA .
nov_chick       DPMSEAKI. .
ibp3_human      . . . . .
ccn-4           . . . . .

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FIG. 2